



SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Beach, David H.
Demetrick, Douglas J.
Serrano, Manuel
Hannon, Gregory J.

(ii) TITLE OF INVENTION: Cell-Cycle Regulatory Proteins, and
Uses Related Thereto

(iii) NUMBER OF SEQUENCES: 35

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Ropes & Gray
(B) STREET: One International Place
(C) CITY: Boston
(D) STATE: MA
(E) COUNTRY: USA
(F) ZIP: 02110

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: WordPad

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US 09/016,869
(B) FILING DATE: 30-JAN-1998

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/893,274
(B) FILING DATE: 15-JUL-1994

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/306,511
(B) FILING DATE: 14-SEP-1994

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/248,812
(B) FILING DATE: 25-MAY-1994

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/227,371
(B) FILING DATE: 14-APR-1994

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/154,915
(B) FILING DATE: 18-NOV-1993

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 07/991,997
(B) FILING DATE: 17-DEC-1992

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Vincent, Matthew P.
(B) REGISTRATION NUMBER: 36,709

(C) REFERENCE/DOCKET NUMBER: GPCI-P10-071

(ix) TELECOMMUNICATION INFORMATION:
 (A) TELEPHONE: (617) 951-7739
 (B) TELEFAX: (617) 951-7050

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 994 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 41..508

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

AAAATAAAAT TATTTCATT CATTCACTCA AAAAAA

994

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 156 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Asp Pro Ala Ala Gly Ser Ser Met Glu Pro Ser Ala Asp Trp Leu
1 5 10 15
Ala Thr Ala Ala Ala Arg Gly Arg Val Glu Glu Val Val Arg Ala Leu Leu
20 25 30
Glu Ala Val Ala Leu Pro Asn Ala Pro Asn Ser Tyr Gly Arg Arg Pro
35 40 45
Ile Gln Val Met Met Met Gly Ser Ala Arg Val Ala Glu Leu Leu Leu
50 55 60
Leu His Gly Ala Glu Pro Asn Cys Ala Asp Pro Ala Thr Leu Thr Arg
65 70 75 80
Pro Val His Asp Ala Ala Arg Glu Gly Phe Leu Asp Thr Leu Val Val
85 90 95
Leu His Arg Ala Gly Ala Arg Leu Asp Val Arg Asp Ala Trp Gly Arg
100 105 110
Leu Pro Val Asp Leu Ala Glu Glu Leu Gly His Arg Asp Val Ala Arg
115 120 125
Tyr Leu Arg Ala Ala Ala Gly Gly Thr Arg Gly Ser Asn His Ala Arg
130 135 140
Ile Asp Ala Ala Glu Gly Pro Ser Asp Ile Pro Asp
145 150 155

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 837 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 328..738

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

| | |
|---|-----|
| GAGGACTCCG CGACGGTCCG CACCCTGCGG CCAGAGCGGC TTTGAGCTCG GCTGCTTCCG | 60 |
| CGCTAGGCGC TTTTCCCAG AAGCAATCCA GGCGCGCCCG CTGGTTCTTG AGCGCCAGGA | 120 |
| AAAGCCCGGA GCTAACGACC GGCGCTCGG CACTGCACGG GGCCCCAAGC CGCAGAAGAA | 180 |
| GGACGACGGG AGGTTAATGA AGCTGAGCCC AGGTCTCCTA GGAAGGAGAG AGTGGCCCGG | 240 |
| AGCAGCGTGG GAAAGAAGGG AAGAGTGTG TTAAGTTTAC GGCCAACGGT GGATTATCCG | 300 |
| GGCCGCTGCG CGTCTGGGGG CTGCGGA ATG CGC GAG GAG AAC AAG GGC ATG | 351 |
| Met Arg Glu Glu Asn Lys Gly Met | |
| 1 5 | |
| CCC AGT GGG GGC GGC AGC GAT GAG GGT CTG GCC ACG CCG GCG CGG GGA | 399 |
| Pro Ser Gly Gly Ser Asp Glu Gly Leu Ala Thr Pro Ala Arg Gly | |
| 10 15 20 | |
| CTA GTG GAG AAG GTG CGA CAC TCC TGG GAA GCC GGC GCG GAT CCC AAC | 447 |

| | | | | |
|---|-----|-----|-----|-----|
| Leu Val Glu Lys Val Arg His Ser Trp Glu Ala Gly Ala Asp Pro Asn | | | | |
| 25 | 30 | 35 | 40 | |
| GGA GTC AAC CGT TTC GGG AGG CGC GCG ATC CAG GTC ATG ATG ATG GGC | | | | 495 |
| Gly Val Asn Arg Phe Gly Arg Arg Ala Ile Gln Val Met Met Met Gly | | | | |
| 45 | 50 | 55 | | |
| AGC GCC CGC GTG GCG GAG CTG CTG CTG CTC CAC GGC GCG GAG CCC AAC | | | | 543 |
| Ser Ala Arg Val Ala Glu Leu Leu Leu His Gly Ala Glu Pro Asn | | | | |
| 60 | 65 | 70 | | |
| TGC GCA GAC CCT GCC ACT CTC ACC CGA CCG GTG CAT GAT GCT GCC CGG | | | | 591 |
| Cys Ala Asp Pro Ala Thr Leu Thr Arg Pro Val His Asp Ala Ala Arg | | | | |
| 75 | 80 | 85 | | |
| GAG GGC TTC CTG GAC ACG CTG GTG GTG CTG CAC CGG GCC GGG GCG CGG | | | | 639 |
| Glu Gly Phe Leu Asp Thr Leu Val Val Leu His Arg Ala Gly Ala Arg | | | | |
| 90 | 95 | 100 | | |
| CTG GAC GTG CGC GAT GCC TGG GGT CGT CTG CCC GTG GAC TTG GCC GAG | | | | 687 |
| Leu Asp Val Arg Asp Ala Trp Gly Arg Leu Pro Val Asp Leu Ala Glu | | | | |
| 105 | 110 | 115 | 120 | |
| GAG CGG GGC CAC CGC GAC GTT GCA GGG TAC CTG CGC ACA GCC ACG GGG | | | | 735 |
| Glu Arg Gly His Arg Asp Val Ala Gly Tyr Leu Arg Thr Ala Thr Gly | | | | |
| 125 | 130 | 135 | | |
| GAC TGACGCCAGG TTCCCCAGCC GCCCACAAACG ACTTTATTCTT CTTACCCAAT | | | | 788 |
| Asp | | | | |
| TTCCCCACCCCC CACCCACCTA ATTGATGAA GGCTGCCAAC GGGGAGCGG | | | | 837 |

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 137 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

| | | | | |
|---|-----|-----|----|--|
| Met Arg Glu Glu Asn Lys Gly Met Pro Ser Gly Gly Ser Asp Glu | | | | |
| 1 | 5 | 10 | 15 | |
| Gly Leu Ala Thr Pro Ala Arg Gly Leu Val Glu Lys Val Arg His Ser | | | | |
| 20 | 25 | 30 | | |
| Trp Glu Ala Gly Ala Asp Pro Asn Gly Val Asn Arg Phe Gly Arg Arg | | | | |
| 35 | 40 | 45 | | |
| Ala Ile Gln Val Met Met Gly Ser Ala Arg Val Ala Glu Leu Leu | | | | |
| 50 | 55 | 60 | | |
| Leu Leu His Gly Ala Glu Pro Asn Cys Ala Asp Pro Ala Thr Leu Thr | | | | |
| 65 | 70 | 75 | 80 | |
| Arg Pro Val His Asp Ala Ala Arg Glu Gly Phe Leu Asp Thr Leu Val | | | | |
| 85 | 90 | 95 | | |
| Val Leu His Arg Ala Gly Ala Arg Leu Asp Val Arg Asp Ala Trp Gly | | | | |
| 100 | 105 | 110 | | |
| Arg Leu Pro Val Asp Leu Ala Glu Arg Gly His Arg Asp Val Ala | | | | |
| 115 | 120 | 125 | | |
| Gly Tyr Leu Arg Thr Ala Thr Gly Asp | | | | |
| 130 | 135 | | | |

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 853 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 213..587

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

| | |
|--|-----|
| GGAGTACAGC AGCGGGAGCA TGGGTCGCAG GTTCTTGGTC ACTGTAAGGA TTCAGCGCGC | 60 |
| GGGCCGCCCA CTCCAAGAGA GGGTTTCTT GGTGAAGTTC GTGCGATCCC GGAGACCCAG | 120 |
| GACAGCGAGC TGCGCTCTGG CTTTCGTGAA CATGTTGTTG AGGCTAGAGA GGATCTTGAG | 180 |
| AAGAGGGCCG CACCGGAATC CTGGACCAGG TG ATG ATG ATG GGC AAC GTT CAC Met Met Met Gly Asn Val His | 233 |
| 1 5 | |
| GTA GCA GCT CTT CTG CTC AAC TAC GGT GCA GAT TCG AAC TGC GAG GAC Val Ala Ala Leu Leu Asn Tyr Gly Ala Asp Ser Asn Cys Glu Asp | 281 |
| 10 15 20 | |
| CCC ACT ACC TTC TCC CGC CCG GTG CAC GAC GCA GCG CGG GAA GGC TTC Pro Thr Thr Phe Ser Arg Pro Val His Asp Ala Ala Arg Glu Gly Phe | 329 |
| 25 30 35 | |
| CTG GAC ACG CTG GTG GTG CTG CAC GGG TCA GGG GCT CGG CTG GAT GTG Leu Asp Thr Leu Val Val Leu His Gly Ser Gly Ala Arg Leu Asp Val | 377 |
| 40 45 50 55 | |
| CGC GAT GCC TGG GGT CGC CTG CCG CTC GAC TTG GCC CAA GAG CGG GGA Arg Asp Ala Trp Gly Arg Leu Pro Leu Asp Leu Ala Gln Glu Arg Gly | 425 |
| 60 65 70 | |
| CAT CAA GAC ATC GTG CGA TAT TTG CGT TCC GCT GGG TGC TCT TTG TGT His Gln Asp Ile Val Arg Tyr Leu Arg Ser Ala Gly Cys Ser Leu Cys | 473 |
| 75 80 85 | |
| TCC GCT GGG TGG TCT TTG TGT ACC GCT GGG AAC GTC GCC CAG ACC GAC Ser Ala Gly Trp Ser Leu Cys Thr Ala Gly Asn Val Ala Gln Thr Asp | 521 |
| 90 95 100 | |
| GGG CAT AGC TTC AGC TCA AGC ACG CCC AGG GCC CTG GAA CTT CGC GGC Gly His Ser Phe Ser Ser Thr Pro Arg Ala Leu Glu Leu Arg Gly | 569 |
| 105 110 115 | |
| CAA TCC CAA GAG CAG AGC TAAATCCGCC TCAGCCCGCC TTTTTCTTCT | 617 |
| Gln Ser Gln Glu Gln Ser | |
| 120 125 | |
| TAGCTTCACT TCTAGCGATG CTAGCGTGTG TAGCATGTGG CTTTAAAAAA TACATAATAA | 677 |
| TGCTTTTTT GCAATCACGG GAGGGAGGAG AGGGAGGGAG CAGAAGGAGG GAGGGAGGGA | 737 |
| GGGAGGGACC TGGACAGGAA AGGAATGGCA TGAGAAACTG AGCGAAGGCG GCCGCGAAGG | 797 |
| GAATAATGGC TGGATTGTTT AAAAAAATAA AATAAAGATA CTTTTAAAAA TGTCAA | 853 |

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 125 amino acids
- (B) TYPE: amino acid
- (C) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met Met Met Gly Asn Val His Val Ala Ala Leu Leu Leu Asn Tyr Gly
1 5 10 15

Ala Asp Ser Asn Cys Glu Asp Pro Thr Thr Phe Ser Arg Pro Val His
20 25 30

Asp Ala Ala Arg Glu Gly Phe Leu Asp Thr Leu Val Val Leu His Gly
35 40 45

Ser Gly Ala Arg Leu Asp Val Arg Asp Ala Trp Gly Arg Leu Pro Leu
50 55 60

Asp Leu Ala Gln Glu Arg Gly His Gln Asp Ile Val Arg Tyr Leu Arg
65 70 75 80

Ser Ala Gly Cys Ser Leu Cys Ser Ala Gly Trp Ser Leu Cys Thr Ala
85 90 95

Gly Asn Val Ala Gln Thr Asp Gly His Ser Phe Ser Ser Ser Thr Pro
100 105 110

Arg Ala Leu Glu Leu Arg Gly Gln Ser Gln Glu Gln Ser
115 120 125

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 231 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..231

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

| | |
|---|-----|
| GCA CTC CTG GAA GCC GGC GCA GAT CCC AAC GCC CTG AAC CGC TTC GGG | 48 |
| Ala Leu Leu Glu Ala Gly Ala Asp Pro Asn Ala Leu Asn Arg Phe Gly | |
| 1 5 10 15 | |
| AGG CGC CCA ATC CAG GTC ATG ATG GGC AGC GCC AGG GTG GCA GAG | 96 |
| Arg Arg Pro Ile Gln Val Met Met Gly Ser Ala Arg Val Ala Glu | |
| 20 25 30 | |
| CTG CTG CTG CTC CAC GGA GCA GAA CCC AAC TGC GCC GAC CCT GCC ACC | 144 |
| Leu Leu Leu His Gly Ala Glu Pro Asn Cys Ala Asp Pro Ala Thr | |
| 35 40 45 | |
| CTT ACC AGA CCT GTG CAC GAC GCA GCT CGG GAA GGC TTC CTG GAC ACG | 192 |

Leu Thr Arg Pro Val His Asp Ala Ala Arg Glu Gly Phe Leu Asp Thr
50 55 60
CTT GTC GTG CTG CAC CGG GCA GGG GCG CGG TTG GAT GTG
Leu Val Val Leu His Arg Ala Gly Ala Arg Leu Asp Val
65 70 75

231

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 77 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Ala Leu Leu Glu Ala Gly Ala Asp Pro Asn Ala Leu Asn Arg Phe Gly
1 5 10 15
Arg Arg Pro Ile Gln Val Met Met Gly Ser Ala Arg Val Ala Glu
20 25 30
Leu Leu Leu His Gly Ala Glu Pro Asn Cys Ala Asp Pro Ala Thr
35 40 45
Leu Thr Arg Pro Val His Asp Ala Ala Arg Glu Gly Phe Leu Asp Thr
50 55 60
Leu Val Val Leu His Arg Ala Gly Ala Arg Leu Asp Val
65 70 75

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 303 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Met Ala Thr Ser Arg Tyr Glu Pro Val Ala Glu Ile Gly Val Gly Ala
1 5 10 15
Tyr Gly Thr Val Tyr Lys Ala Xaa Asp Pro His Ser Gly His Phe Val
20 25 30
Ala Leu Lys Ser Val Arg Val Pro Asn Gly Gly Gly Gly Gly Gly
35 40 45
Leu Pro Ile Ser Thr Val Arg Glu Val Ala Leu Leu Arg Arg Leu Glu
50 55 60
Ala Phe Glu His Pro Asn Val Val Arg Leu Met Asp Val Cys Ala Thr
65 70 75 80

Ser Arg Thr Asp Arg Glu Ile Lys Val Thr Leu Val Phe Glu His Val
85 90 95

Asp Gln Asp Leu Arg Thr Tyr Leu Asp Lys Ala Pro Pro Pro Gly Leu
100 105 110

Pro Ala Glu Thr Ile Lys Asp Leu Met Arg Gln Phe Leu Arg Gly Leu
115 120 125

Asp Phe Leu His Ala Asn Cys Ile Val His Arg Asp Leu Lys Pro Glu
130 135 140

Asn Ile Leu Val Thr Ser Gly Gly Thr Val Lys Leu Ala Asp Phe Gly
145 150 155 160

Leu Ala Arg Ile Tyr Ser Tyr Gln Met Ala Leu Thr Pro Val Val Val
165 170 175

Thr Leu Trp Tyr Arg Ala Pro Glu Val Leu Leu Gln Ser Thr Tyr Ala
180 185 190

Thr Pro Val Asp Met Trp Ser Val Gly Cys Ile Phe Ala Glu Met Phe
195 200 205

Arg Arg Lys Pro Leu Phe Cys Gly Asn Ser Glu Ala Asp Gln Leu Gly
210 215 220

Lys Ile Phe Asp Leu Ile Gly Leu Pro Pro Glu Asp Asp Trp Pro Arg
225 230 235 240

Asp Val Ser Leu Pro Arg Gly Ala Phe Pro Pro Arg Gly Pro Arg Pro
245 250 255

Val Gln Ser Val Val Pro Glu Met Glu Glu Ser Gly Ala Gln Leu Leu
260 265 270

Leu Glu Met Leu Thr Phe Asn Pro His Lys Arg Ile Ser Ala Phe Arg
275 280 285

Ala Leu Gln His Ser Tyr Leu His Lys Asp Glu Gly Asn Pro Glu
290 295 300

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 326 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Met Glu Lys Asp Gly Leu Cys Arg Ala Asp Gln Gln Tyr Glu Cys Val
1 5 10 15

Ala Glu Ile Gly Glu Gly Ala Tyr Gly Lys Val Phe Lys Ala Xaa Asp

20 25 30

Leu Lys Asn Gly Gly Arg Phe Val Ala Leu Lys Arg Val Arg Val Gln
35 40 45

Thr Gly Glu Glu Gly Met Pro Leu Ser Thr Ile Arg Glu Val Ala Val
50 55 60

Leu Arg His Leu Glu Thr Phe Glu His Pro Asn Val Val Arg Leu Phe
65 70 75 80

Asp Val Cys Thr Val Ser Arg Thr Asp Arg Glu Thr Lys Leu Thr Leu
85 90 95

Val Phe Glu His Val Asp Gln Asp Leu Thr Thr Tyr Leu Asp Lys Val
100 105 110

Pro Glu Pro Gly Val Pro Thr Glu Thr Ile Lys Asp Met Met Phe Gln
115 120 125

Leu Leu Arg Gly Leu Asp Phe Leu His Ser His Arg Val Val His Arg
130 135 140

Asp Leu Lys Pro Gln Asn Ile Leu Val Thr Ser Ser Gly Gln Ile Lys
145 150 155 160

Leu Ala Asp Phe Gly Leu Ala Arg Ile Tyr Ser Phe Gln Met Ala Leu
165 170 175

Thr Ser Val Val Val Thr Leu Trp Tyr Arg Ala Pro Glu Val Leu Leu
180 185 190

Gln Ser Ser Tyr Ala Thr Pro Val Asp Leu Trp Ser Val Gly Cys Ile
195 200 205

Phe Ala Glu Met Phe Arg Arg Lys Pro Leu Phe Arg Gly Ser Ser Asp
210 215 220

Val Asp Gln Leu Gly Lys Ile Leu Asp Val Ile Gly Leu Pro Gly Glu
225 230 235 240

Glu Asp Trp Pro Arg Asp Val Ala Leu Pro Arg Gln Ala Phe His Ser
245 250 255

Lys Ser Ala Gln Pro Ile Glu Lys Phe Val Thr Asp Ile Asp Glu Leu
260 265 270

Gly Lys Asp Leu Leu Lys Cys Leu Thr Phe Asn Pro Ala Lys Arg
275 280 285

Ile Ser Ala Tyr Ser Ala Leu Ser His Pro Tyr Phe Gln Asp Leu Glu
290 295 300

Arg Cys Lys Glu Asn Leu Asp Ser His Leu Pro Pro Ser Gln Asn Thr
305 310 315 320

Ser Glu Leu Asn Thr Ala
325

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 85 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Met Met Met Gly Xaa Xaa Xaa Val Ala Xaa Leu Leu Leu Xaa Xaa Gly
1 5 10 15
Ala Xaa Xaa Asn Cys Xaa Asp Pro Xaa Thr Xaa Xaa Xaa Arg Pro Val
20 25 30
His Asp Ala Ala Arg Glu Gly Phe Leu Asp Thr Leu Val Val Leu His
35 40 45
Xaa Xaa Gly Ala Arg Leu Asp Val Arg Asp Ala Trp Gly Arg Leu Pro
50 55 60
Xaa Asp Leu Ala Xaa Glu Xaa Gly His Xaa Asp Xaa Xaa Xaa Tyr Leu
65 70 75 80
Arg Xaa Ala Xaa Gly
85

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 157 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Met Asp Pro Ala Ala Gly Ser Ser Met Glu Pro Ser Ala Asp Trp Leu
1 5 10 15
Ala Thr Ala Ala Ala Arg Gly Arg Val Glu Glu Val Arg Ala Leu Leu
20 25 30
Glu Ala Val Ala Leu Pro Asn Ala Pro Asn Ser Tyr Gly Arg Arg Pro
35 40 45
Ile Gln Val Met Met Met Gly Xaa Xaa Xaa Val Ala Xaa Leu Leu Leu
50 55 60

Xaa Xaa Gly Ala Xaa Xaa Asn Cys Xaa Asp Pro Xaa Thr Xaa Xaa Xaa
65 70 75 80

Arg Pro Val His Asp Ala Ala Arg Glu Gly Phe Leu Asp Thr Leu Val
85 90 95

Val Leu His Xaa Xaa Gly Ala Arg Leu Asp Val Arg Asp Ala Trp Gly
100 105 110

Arg Leu Pro Xaa Asp Leu Ala Xaa Glu Xaa Gly His Xaa Asp Xaa Xaa
115 120 125

Xaa Tyr Leu Arg Xaa Ala Xaa Gly Gly Thr Arg Gly Ser Asn His Ala
130 135 140

Arg Ile Asp Ala Ala Glu Gly Pro Ser Asp Ile Pro Asp
145 150 155

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 138 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Met Arg Glu Glu Asn Lys Gly Met Pro Ser Gly Gly Ser Asp Glu
1 5 10 15

Gly Leu Ala Thr Pro Ala Arg Gly Leu Val Glu Lys Val Arg His Ser
20 25 30

Trp Glu Ala Gly Ala Asp Pro Asn Gly Val Asn Arg Phe Gly Arg Arg
35 40 45

Ala Ile Gln Val Met Met Gly Xaa Xaa Xaa Val Ala Xaa Leu Leu
50 55 60

Leu Xaa Xaa Gly Ala Xaa Xaa Asn Cys Xaa Asp Pro Xaa Thr Xaa Xaa
65 70 75 80

Xaa Arg Pro Val His Asp Ala Ala Arg Glu Gly Phe Leu Asp Thr Leu
85 90 95

Val Val Leu His Xaa Xaa Gly Ala Arg Leu Asp Val Arg Asp Ala Trp
100 105 110

Gly Arg Leu Pro Xaa Asp Leu Ala Xaa Glu Xaa Gly His Xaa Asp Xaa
115 120 125

Xaa Xaa Tyr Leu Arg Xaa Ala Xaa Gly Asp
130 135

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 127 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Met Met Met Gly Xaa Xaa Xaa Val Ala Xaa Leu Leu Leu Xaa Xaa Gly
1 5 10 15

Ala Xaa Xaa Asn Cys Xaa Asp Pro Xaa Thr Xaa Xaa Xaa Arg Pro Val
20 25 30

His Asp Ala Ala Arg Glu Gly Phe Leu Asp Thr Leu Val Val Leu His
35 40 45

Xaa Xaa Gly Ala Arg Leu Asp Val Arg Asp Ala Trp Gly Arg Leu Pro
50 55 60

Xaa Asp Leu Ala Xaa Glu Xaa Gly His Xaa Asp Xaa Xaa Xaa Tyr Leu
65 70 75 80

Arg Xaa Ala Xaa Gly Cys Ser Leu Cys Ser Ala Gly Trp Ser Leu Cys
85 90 95

Thr Ala Gly Asn Val Ala Gln Thr Asp Gly His Ser Phe Ser Ser Ser
100 105 110

Thr Pro Arg Ala Leu Glu Leu Arg Gly Gln Ser Gln Glu Gln Ser
115 120 125

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 17 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Val Ala Glu Ile Gly Xaa Gly Ala Tyr Gly Xaa Val Xaa Lys Ala Arg Asp
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 6 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Val Xaa Lys Ala Arg Asp
1 5

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Lys Ala Arg Asp
1

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 960 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

| | |
|---|-----|
| CGGAGAGGGGA ATT CGGCACGA GGCAGCATG GAGCCTTCGG CTGACTGGCT GGCCACGGCC | 60 |
| GC GGGCCCCGGG GTCGGGTAGA GGAGGTGCGG GCGCTGCTGG AGGCGGTGGC GCTGCCCAA | 120 |
| CGCACCGAAT AGTTACGGTC GGAGGCCGAT CCAGGTCATG GATGATGGGC AGCGCCCCGA | 180 |
| GTGGCGGAGC TGCTGCTGCT CCACGGCGCG GAGCCCAACT GCGCCGACCC CGCCACTCTC | 240 |

| | |
|--|-----|
| ACCCGACCCG TGCACCACGC TGCCCCGGAG GGCTTCTGGA CACGCTGGTG GTGCTGCACC | 300 |
| GGGCCGGGGC GCGGCTGGAC GTGCGCGATG CCTGGGGCCG TCTGCCCGTG GACCTGGCTG | 360 |
| AGGAGCTGGG CCATCGCGAT GTCGCACGGT ACCTGCGCGC CCGTGCAGGG GGCACCAAGAG | 420 |
| GCAGTAACCA TGCCCGCATA GATGCCGCGG AAGGTCCCTC AGACATCCCC GATTGAAAGA | 480 |
| ACCAGAGAGG CTCTGAGAAA CCTCGGGAAA CTTAGATCAT CAGTCACCGA AGGTCCCTACA | 540 |
| GGGCCACAAC TGCCCCGCC ACAACCCACC CCGCTTCGT AGTTTCATT TAGAAAATAG | 600 |
| AGCTTTAAA AATGTCCTGC CTTTTAACGT AGATATAAGC CTTCCCCCAC TACCGTAAAT | 660 |
| GTCCATTAT ATCATTTTT ATATATTCTT ATAAAAATGT AAAAAAAGAA AACACCGCT | 720 |
| TCTGCCTTT CACTGTGTTG GAGTTTCTG GAGTGAGCAC TCACGCCCTA AGCGCACATT | 780 |
| CATGTGGCA TTTCTTGCAG GCCTCGCAGC CTCCGGAAGC TGTCGACTTC ATGACAAGCA | 840 |
| TTTTGTGAAC TAGGGAAAGCT CAGGGGGGTT ACTGGCTTCT CTTGAGTCAC ACTGCTAGCA | 900 |
| AATGGCAGAA CCAAAGCTCA AATAAAAATA AAATTATTTT CATTCAATTCA CTCAAAAAAA | 960 |

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 334 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

| | |
|---|-----|
| GGNGGNAAGN TGTGGGGGAA AGTTTGGGGA TGGAANACCA ANCCCTCCTT TCNTTACCAA | 60 |
| ACNCTGGCTC TGNCAGGCT NCNTCCGANT GGTNCCCCG GGGGAGACCC AACCTGGGN | 120 |
| GACTTCAGGG NTGCNACATT CATTCACTAA GTGCTNGGAG NTAATANCAC CTCCTCCGAG | 180 |
| CANNGACAGG NTGGAGGGG GCTCTTCCCC CANCACCGGA GGAAGAAAGA GGAGGGNCTN | 240 |
| CGGAGAGGGG GAGAACAGAC AACGGGCGGC GGGGAGCAGC ATGGATCCGG CGGCAGGGAG | 300 |
| CAGCATGGAN CCTTCGACTG ACTGACTGCC TCGC | 334 |

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 368 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

| | |
|---|-----|
| TCNCTTATTG NTAGGANATA ATAACACCTC CACCGATAAC TTCACTTACA ACGTCCNNNT | 60 |
| TCCTGGAAAG ATACACAGCG TTCCCTCCAG AGGATTTGTG GGACAGGGTN GGAGNGGTCT | 120 |
| CTTCCNCCAC CACCGGAGGA AGAAAGAGGA GGGGCTGNCT GTTCACCAGA GGGTGGGACG | 180 |
| GACCNCGTAC GCTCGNCNC TNCGGAGAGG GGGAGAGCAT CANCGGNCGN CGGGGAGCAA | 240 |
| CATGGAACCG NCGGCGGGGA GCAGCATGGA NCCTTCGGCT GACTGGCTGN CCACGNCCAC | 300 |
| GNCCCGGGGT CGGGTAGAGG AGGTGCGGNC GCTNCTGGAG GCGGGGNCTC TGNCCAACNC | 360 |
| GCTAAAAN | 368 |

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 404 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

| | |
|---|-----|
| GACNNNCTCC GGCCGGNGTC GGGTAGAGGA GGTGCGGGCG CTGCTGGAGG CGGGGGCGCT | 60 |
| GCCCAACGCA CCGAATAGTT ACGGTCGGAG GCCGATCCAG GTNNGGGTAG AGGGTCTGCA | 120 |
| GCGGGAGCAG GGGATGGCGG GCGACTCTGG AGGACGAAGT TTGCAGGGGA ATTGGAATCA | 180 |
| GGTAGCGCTT CGATTCTCCN GAAAAAGGGG AGGCTTCCTG GGGAGTTTC AGAAGGGGTT | 240 |
| TGTAATCACA GACCTCCTCC TGGCGACGTC CTGGGGGCTT GGGAGCCAA GGAAGAGGAA | 300 |
| TNAGGAGCCA CGCGCGTACG AGTCTCTCGA ATGCTGAGAA GATCTNAAGG GGGAACATA | 360 |
| TTTGTATTAG CNTCCAAGTN TNCTCTNTAT CANATACAAA NTNC | 404 |

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 401 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

| | |
|---|-----|
| CTCTNANCCC GGGTAGAGGG TCTGCAGCGG GAGCAGNGGA TGGCGGGCGA CTCTGGAGGA | 60 |
| CGAAGTTGGC AGGGGAATTG GAATCAGGTA GCGCTTCGAN TCTCCGGAAA AAGGGGAGGC | 120 |
| TTCCTGGGA GTTNNCAGAA GGGGTTTGTA ATCACAGNCC TCCNCCTGGC GACGCCCTGG | 180 |
| GGGGTTGGGA AGCCAAGGAA GAGGAATGAG GAGNCACGCG CNTACAGNTC TCTCGAATNC | 240 |
| TGANAAGATC TGAAGGGGG AACATATTTG TATTAGNATN NAAGTATGCT CTTTATCAGA | 300 |
| TAGAAAATTC ACGAACGTGT GGNATAAAA GGGAGTCTTA AAGAAATNTA AGATGTGCTG | 360 |
| GGACTACTTA GCCTCCAANA CACAGATNCC TGGATGGAGC T | 401 |

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 459 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

| | |
|---|-----|
| AAAANAAAAA AAAATCTCCC AGGCCTAACAA TAATTNTCAAG GAAAGAAATT TCAGTAGTTG | 60 |
| NATCTCAGGG GAAATACAGG AAGTTAGCCT GGAGTAAAAG TCAGTGTGTC CCTGCCCTT | 120 |
| TGCTANATTG CCCGTGCCTC ACAGTGCTCT CTGCCTGTGA CGACAGCTCC NCAGAAGTTC | 180 |
| GGAGGATATA ATGGAATTCA TTGTGTACTG AAGAATGGAT AGAGAACTCA AGAAGGAAAT | 240 |
| TGGAAACTGG AAGCAAATGT AGGGGTAATT AGACACCTGG GGCTTCTGTG GGGTCTGCT | 300 |
| TGGCGGTGAG GGGGCTCTAC ACAAGCTTCC TTTCCGTCAT GCGNNCCCC ACCCTGGCTC | 360 |
| TGACCATTCT GTTCTCTCTG GCAGGTCATG ATGATGGCA GCGCCCGAGG CGCGGAGCTG | 420 |
| CTGCTGCTCC ACGGCGCGGA GCCCACTGCT CCGACGCCG | 459 |

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 390 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

| | |
|--|-----|
| AANAAAAAAAG AAATNGATAA NATAGAGGAA TGAACANATT AAAATCAAAA AACANAACAN | 60 |
| AGACATAATA AAAAACGAGA ATGTTCTAGA CNTAATCATA ATTATAAAGC TCAAGACTCA | 120 |
| TTGATATNAA GGADATTGAA GGGAAATCTT AACTAGCACA ANNGNATNAA AAAANAATTG | 180 |
| CCACGACACC GCCACTCTCA ACGCATCCGT GCTCGACACT GCCCGGGAGG TCNTCCTGGA | 240 |
| CACGCTGGTG GTNCTCCACC GGNCCGGGC ACGTCTGGAC GTGCGCGATG CCTGGGNCCG | 300 |
| NCTACCCGTG GTACCTGACT GAGGACCTGG GCCATCCCGA TTTCGCNNGG TANCTCNNGN | 360 |
| GGCTGNNGGG GCCAANAGAG GNCANTACCC | 390 |

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 214 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

| | |
|--|-----|
| CCTGCNACGA CCCCGCCACT CTCACCCGAC CCGTGCACGA CGCTGTCCGG GAGGGTTTCC | 60 |
| TGGACACGCT GGTGGTGCTG CACCGGGCCG GGGNGCGGTT GGACGTGCGC GATGCCCTGGG | 120 |
| GCCGCCTNCC CGTGGNACCT GGTTGAGGAG CTGGGNACATC GCGATGTCGC ACGGTACCTG | 180 |
| CGCGCGTTGC GGGGGGCACC AGAGGNNAGT NACC | 214 |

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 235 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

| | |
|--|-----|
| NCTCTCACGG TGGGGAGGCC AACTGCGCCG AACCCGCCAC TCTCACCCGA CCCGCGCACG | 60 |
| ACGGTGCCCG GGAGGGGTTTC CTGGACACGC TGTTGGTGCT GCACCGGGCC GGGGCCCGC | 120 |
| TGGACGTTCG NGATGCCTGG GGGNTCTNTC CGTNGNACCT GGCTGAAGAG CTGGNNACATC | 180 |
| GNGATGTCGC ACGGCCNCTG TGTGNGGNTG CGGGGGCAC CATAGGTCAG TNTCC | 235 |

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 573 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

| | |
|--|-----|
| NAAGTATGAG CGAACNAAT TGTGGTTGAA GAANAGGAA TCGTAGGGAA CTTCGGGATC | 60 |
| CCNCNGGGAN CNCCAGAACCC TGAGNCGCCN ATTGGAAATN ACAAACTGNC TGNATCACTC | 120 |
| CGNACCAGGT NCAAAAGATA CCTGGGGANG CGGGAAGGGA AAGACNACAT CNAGACGCC | 180 |
| TTCGCNCCTN GGNATTGTGA GCAGCCTCTG AGACTCATTN ATATNACACT CTCGTNTTC | 240 |
| TTCTTACAAC CCTGCGGNCC GCGCGGTGCG GCTTTCTCTG CCCTCCGCCG GGTGGACCTG | 300 |
| GAGCGCTTGA GCGGTCGGCG CGCCTGGAGC AGCCAGGC GG NCAGTGGACT AGCTGCTGGA | 360 |
| CCAGGGAGGT GTGGGAGAGC GGTGGCGCG GGTACATGCA CGTGAAGCCA TTGCGAGAAC | 420 |
| TTTATCCATA AGTATTTCAA TACCGGTAGG GACGGCAAGA GAGGAGGGCG GGATGTGCCA | 480 |
| CACATTTG ACCTCAGGTT TCTAACGCCCT GTTTCTTC TGCCCTCTGC AGACAACCCC | 540 |
| CGATTGAAAG AACCAAGAGAG GCTCTGAGAA ACC | 573 |

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 434 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

| | |
|---|-----|
| CCCCATCGCG CCTTGGGANT GTGAGCNACC ATTGAGACTC ATNAATATAG CACTCGTTT | 60 |
| TCTTCTTGCA ACCCTGCCCN CGCGCGGTC GCGCTNTCTC TGCCCTCCGC NGGGTGGACC | 120 |
| TGGAGCGAGC GCTTGAGCGG TCGGTGGCG CGCCTGGANC AGCCAGGC GG AGCTGGACT | 180 |
| ACCTNCTGGA CCAGGGACCT GTGGGAGAGC GGTGNCGCG GGTACATGCA CGTGAAGCCA | 240 |
| TTGCGAGAAC TTTATCCATA AGTATTTCAA TGCCGGTAGG GACGGCAAGA GAGGAGGGCG | 300 |

| | |
|---|-----|
| GGATGTNCCA CACATCTTG ACCTCAGGTT TCTAACGCCT GTTTTCTTTC TGCCCTCTGC | 360 |
| AGACATCCCC GATTGAAAGA ACCAGAGAGG CTCTGAGAAA CCTCCGGAAA CTTAGNTCAT | 420 |
| CANTCGCCGN AAAA | 434 |

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 502 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

| | |
|--|-----|
| AGAAATTAGA TCATCAGTCA CCGATCCTCC TACAGGGNCA CAACTGNCCC CGCCACAACC | 60 |
| CACCCCGNTT TCGTAGTTT CATTTAGAAA ATAGAGCTTT TAAAAATGTC CTGCCTTTA | 120 |
| ACGTAGATAT ATGCCTTCCC CCACTACCGN AAATGTCCAT TTATATCATN TTTTATATAT | 180 |
| TCTTATAAAA ATGTAAAAAA GAAAAACACC GCTTCTGCCT TTTCACTGTG TTGGAGTTT | 240 |
| CTGGAGTGAG CACTCACGCC CTAAGGCCAC ATTCACTGTGG GCATTTCTTG CGAGCCTCGC | 300 |
| AGNCTCCGGA AGCTGTCGAC CTCGAGGGGG GGNCCGGTAC CCAATTGCCC CTATAGTGAG | 360 |
| TCGTATTACA ATTCACTGGN CGNCGNTTT ACAACGTCGG TGGACTGGGA AAACCCGGN | 420 |
| GTTACCCAAC TTTAATCGNC TTGGAGGACA TCCCCCTTT CGCCAGNTGG GGTTATAGNG | 480 |
| AAGAGGGCCN CACCNNTCGC CC | 502 |

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 503 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

| | |
|---|-----|
| CANCNATNTN CGGCATTTCT NGNGAGCCTC GTAGTCTCCG GATGNTGTCG ACCTCGAGGG | 60 |
| GGGGNCCNGT ACCCAATTG NCCTATNGTG AGTCGTNTTA CAATTCACTG GCCGCCGTTT | 120 |
| TNACAAACGTC GNTGNACTGG GAAAACCTG GTGTTACCCA ACTTNAATGT CCTTGNAGNA | 180 |
| CATCCCCCTT TNCGCCAGCT GGTGTAATAG CGANGAGGCC CGCACCGATC GCCCTTCCCA | 240 |

| | |
|--|-----|
| ACAGTTGNGC AGCCTGAATG GCGAATGGAA ATTGTAAGCG TTAATATTTT GTTAAAATT | 300 |
| GCGTTANATC NTCGGTTAAN TCAGCTCATN TTTTATCCAA TAGGCCGANA TCGGCANAAT | 360 |
| CCCCAATAAA TCAANAGAAT AGACCGAGAT AGGGTTGAGT GTCGTTCCAG TTNGGGAAACA | 420 |
| NGAGTCCACT ATAAAGANC GTAGNCTCNA ACGTCANAGG GCGAAAAAACC NTNTTCAGN | 480 |
| GGATTGGNCC ACTACGCNTA NCC | 503 |

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 515 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

| | |
|--|-----|
| CANCNATNTN CGGCATTCT NGNGAGCCTC GTAGTCTCCG GATGNTGTG ACCTCGAGGG | 60 |
| GGGGNCCNGT ACCCAATTG NCCTATNGTG AGTCGTNTTA CAATTCACTG GCCGCCGTT | 120 |
| TNACAACGTC GNTGNACTGG GAAAACCCTG GTGTTACCCA ACTTNAATCG CCTTGNAGNA | 180 |
| CATCCCCCTT TNCGCCAGCT GGTGTAATAG CGANGAGGCC CGCACCGATC GCCCTTCCA | 240 |
| ACAGTTGNGC AGCCTGAATG GCGAATGGAA ATTGTAAGCG TTAATATTTT GTTAAAATT | 300 |
| GCGTTANATC NTCGGTTAAN TCAGCTCATN TTTTATCCAA TAGGCCGANA TCGGCANAAT | 360 |
| CCCCAATAAA TCAANAGAAT AGACCGAGAT AGGGTTGAGT GTCGTTCCAG TTNGGGAAACA | 420 |
| NGAGTCCACT ATAAAGANC GTAGNCTCNA ACGTCANAGG GCGAAAAAACC NTNTTCAGN | 480 |
| GGATTGGNCC ACTACGCNTA NCCATCACCC TATTC | 515 |

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 89 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

Ile Gln Val Met Met Met Gly Ser Ala Arg Val Ala Glu Leu Leu Leu
1 5 10 15

His Gly Ala Glu Pro Asn Cys Ala Asp Pro Ala Thr Leu Thr Arg Pro Val
20 25 30

His Asp Ala Ala Arg Glu Gly Phe Leu Asp Thr Leu Val Val Leu His Arg
35 40 45 50

Ala Gly Ala Arg Leu Asp Val Arg Asp Ala Trp Gly Arg Leu Pro Val Asp
55 60 65

Leu Ala Glu Glu Leu Gly His Arg Asp Val Ala Arg Tyr Leu Arg Ala Ala
70 75 80 85

Ala Gly Gly Thr

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 88 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

Ile Gln Val Met Met Met Gly Ser Ala Arg Val Ala Glu Leu Leu Leu
1 5 10 15

His Gly Ala Glu Pro Asn Cys Ala Asp Pro Ala Thr Leu Thr Arg Pro Val
20 25 30

His Asp Ala Ala Arg Glu Gly Phe Leu Asp Thr Leu Val Val Leu His Arg
35 40 45 50

Ala Gly Ala Arg Leu Asp Val Arg Asp Ala Trp Gly Arg Leu Pro Val Asp
55 60 65

Leu Ala Glu Glu Arg Gly His Arg Asp Val Ala Gly Tyr Leu Arg Thr Ala
70 75 80 85

Thr Gly Asp

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 85 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide